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Result
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Maximum I
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Maximum Match 100%
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Copyright (c) 1993 - 2000 Compugen Ltd
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15.135 Million cell updates/sec

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FSA_HUMAN
CAS2_CAPHI
APA4_MACFA
MTGB_HUMAN
APA5_CAPHI
APA6_MACFA
MTGB_HUMAN
YM3B_YEAST
YMFX_LIPMA
ERB3_RAT
Y192_HUMAN
YT94_HUMAN
TPM2_HUMAN
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AGRP_LUFCY
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Q46941
Q04672
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Q06455
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Q9tt90
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y Match Local Si nes 19;	EMBL; M16891; PSIR; A30838; HSSP; P50477; INTERPRO; IPR PFAM; PF00546 Seed storage SIGNAL CHAIN CHAIN SEQUENCE 58	CONVICILIN. This SWISS-PROT This SWISS-PROT This Swiss-Prot between the Sw the European Bi use by non-pr modified and th entities requir or send an emai	SEQUENCE FROM SEQUENCE FROM CAA. P) "Developmental permination. Y the storage pr plant Mol. Bic -!- FUNCTION: -!- SUBCELLULP BODIES.	GOSHI VCLB_GOSHI VCLB_GOSHI P09801; 01-MAR-1989 01-MAR-1989 15-JUL-1999 VICTLIN C72 Gossypium hi Eukaryota; V Magnoliophyt Malvales; Ma		
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Score 105; DE Pred. No. 0.00 9; Mismatches	1. VICIL1	YCININ, ETC.) 'Is copyright. It is present is present in the present in the present institute. The institutions as long tement is not removed: icense agreement (See icense@isb.sib.ch).	ocki A.B of cott d amino es."; (1986). PROTEIN COTYLEDOR	PRT; 5 ted) sequence up annotation HA-GLOBULIN cotton) Embryophyta; Ons; core eu pium.	ALIO	BTD_DROME EGRR_MOMN HSP1_PIG TPM1_CHICK TPM1_CHICK TPM1_CHICK TPMB_CHICK BMK_DROME GLCX_SOMB MST2_DROHY CALD_MELGA BMH2_YEAST
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01-MAR-1989
01-MAR-1989
15-JUL-1999
        Kimura M., Park S.S., Sakai R., Yamasaki N., Funatsu G.;
"Primary structure of 6.5k-arginine/glutamate-rich polypeptide fi
seeds of sponge gourd (Luffa (2-1)Indrica) ";
Biosci. Biotechnol. Biochem. 61:984-988(1997)
-i- FUNCTION: STORAGE PROTEIN WHICH PROVIDES NITROGEN AND CARBON
RESERVES DURING GERMINATION AND SEEDLING GROWTH.
                                                                                                                                                       15-DEC-1998 (Rel. 37, Created)
15-DEC-1998 (Rel. 37, Last sequence update)
15-DEC-1998 (Rel. 37, Last sequence update)
6.5 KDA ARGININE/GLUTAMATE-RICH POLYPEPTIDE (6.5K-AGRP).
Luffa cylindrica (Smooth loofah) (Sponge gourd).
Eukaryota; Viridiplantae; Embryophyta; Tracheophyta; Spermatophyta;
Magnollophyta; eudicotyledons; core eudicots; Rosidae; eurosids I;
Cucurbitales; Cucurbitaceae; Luffa.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Chian C.A., Borroto K., Kamalay J.A., Dure L. III;

"Developmental biochemistry of cottonseed embryogenesis and germination. XIX. Sequences and genomic organization of the alpha globulin (vicilin) genes of cottonseed.";

Plant Mol. Biol. 9:533-546(1987).

-i- FUNCTION: SEED STORAGE PROTEIN.

-i- SUBCELLULAR LOCATION: COTYLEDONARY MEMBRANE-BOUND VACUOLAR PROTEIN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               PIR;
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modified and this statement is not removed. Usage by an
entities requires a license agreement (See http://www.isb-
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Eukaryota; Viridiplantae; Embryophyta; Tracheophyta; Spermatophyta;
Magnoliophyta; eudicotyledons; core eudicots; Rosidae; eurosids II;
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01-MAR-1989 (Rel. 10, Last sequence update)
15-JUL-1999 (Rel. 38, Last annotation update
VICILIN GC72-A PRECURSOR (ALPHA-GLOBULIN A).
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                                                                                               MEDLINE=97357433; PubMed-9214759;
                                                                                                                 TISSUE-SEED
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SEQUENCE
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Q09662;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Caenorhabditis elegans.
Eukaryota; Metazoa; Nen
Rhabditidae; Peloderina
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androgen
Biochem.
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                                                                                                                                                                                                                                                                                                                                                             Marcelli
McPhaul M
                                                            SEQUENCE OF 468-919 FROM N.A.
MEDLINE-88240407; PubMed-3377788;
Trapman J. Klaassen P. Kuiper G
Faber P.W. van Rooij H.C.J., Geu
                                                                                                                                                                                                                                                                    identification of mutations that cau
termination of the receptor protein
complete androgen resistance.";
Mol. Endocrinol. 4:1105-1116(1990).
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Lubahn D.B., Josep
French F.S., Wilso
                              "Cloning, structure and expression
                                                                                                                      SEQUENCE OF 468-919 FROM
                                                                                                                                                                          Chang C., Kokontis J., Liao "Molecular cloning of human androgen receptors.";
                                                                                                                                                                                                                    SEQUENCE OF 189-919 FROM N.A. MEDLINE=88178111; PubMed=3353726;
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                                                                                                                                                                                                                                                                                                                                          "Definition of the human androgen receptor gene
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Natl. Acad. Sci. U.S.A. 85:7211-7215(1988).
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                                                 E., Brinkmann A
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         and trans-activation by human androgen receptor."; docrinol, 4:417-427/1990
                                                                                                                                                     240:324-326(1988)
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               receptor.
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Joseph D.R., Sar M.,
Wilson E.M.;
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153:241-248(1988)
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Sai T., van Rooij H.C., Kaufman M., Rosenfield R "Substitution of aspartic acid-686 by histidine human androgen receptor leads to a functionally altered hormone-binding characteristics.", Mol. Endocrinol. 5:1562-1569(1991).
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                                                                                                       Ris-Stalpers C., Trifiro M.A., Kuiper G.G., Sai T., van Rooij H.C., Kaufman M., Rosenfi
                                                                                                                          VARIANT CAIS ASN-695 AND HIS-695,
MEDLINE=92131007; PubMed=1775137;
                                                                                                                                                                                    "Androgen resistance associated with a mutation receptor at amino acid 772 (Arg-->Cys) results i decreased messenger ribonucleic acid levels and
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             MEDLINE-97169385; PubMed-9016528; Gottlieb B., Trifiro M., Lumbroso R., "The androgen receptor gene mutations Nucleic Acids Res. 25:158-162(1997).
                     VARIANTS CAIS AND PAIS.
MEDLINE=93338440; Pubmed=1307250;
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Berrevoets C., Claassen E., van
Brinkmann A.O., Mulder E.;
                                                                                                                                                                                                                                                                                receptors from subjects with complete Mol. Endocrinol. 4:1759-1772(1990).
                                                                                                                                                                                                                                                                                                                               Brown
                                                                                                                                                                                                                                                                                                                                          MEDLINE~91186983;
                                                                                                                                                                                                                                                                                                                                                                                      "A mutation in the ligand binding human LNCaP cells affects steroid response to anti-androgens ";
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                                                                                                                                                                          receptor function.
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                                                                                                                                                                                                                                                                                                       "Functional characterization of naturally occurring
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Sleddens H.F., Oostra
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POLYMORPHISM OF POLY-GLN
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                                                                                                                                                               Clin. Endocrinol.
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                                                                                                                                                                                                                                               PubMed=1856263;
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is-Stalpers C.,
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Rooij H.C.J.,
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            H.R.,
                                                                            er G.G., Jenster G., Romalo
Rosenfield R.L., Liao S.;
by histidine or asparagine
functionally inactive prote
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 Mammalia;
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Newmark J.R., Hardy D.O., Tonb D.C., Carter B.S., Epstein J.L.
Isaacs W.B., Brown T.R., Barrack E.R.;
"Androgen receptor gene mutations in human prostate cancer.";
Proc. Natl. Acad. Sci. U.S.A. 89:6319-6323(1992).
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                                                                                                                        ANDR_PANTR O97775;
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MEDLINE-93315568; PubMed-8325932;
Nakao R., Yanase T., Sakai Y., Haji M., Nawata H.;
"A single amino acid substitution (Gly743 --> Val)
                                                                                                                                                                                                                                                                                                                                                                                                     VARIANT CAIS ARG-807.
MEDLINE-94108430; PubMed-8281140;
MEDLINE-94108430; PubMed-8281140;
Adeyemo O., Kallio P.J., Palvimo J.J., Kontula K., Jaenne O.A.;
As single-base substitution in exon 6 of the androgen receptor gene reassing complete androgen insensitivity: the mutated receptor fails to transactivate but binds to DNA in vitro.";
Hum. Mol. Genet. 2:1809-1812(1993).
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[19]
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                           Eukaryota;
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Fukumaki Y., Nawata H.;
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MEDLINE=92235226; PubMed=1569163;
                                                                   ANDROGEN RECEPTOR
                                                                                                                                                                                                                                                                                                                      binding
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                                      troglodytes (Chimpanzee).
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              Eutheria;
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A DNA-BINDING DOMAIN AND A C-TERMINAL STEROID-BINDING DOMAIN.
-!- SIMILARITY: BELONGS TO THE NUCLEAR HORMONE RECEPTORS FAMILY.
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IN TARGET TISSU
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P02319;
                                                          Peschon J.J., Behringer R.R., Brinster R.L., Palm "Spermatid-specific expression of protamine 1 in Proc. Natl. Acad. Sci. U.S.A. 84:5316-5319(1987).
                                                                                                                                                                                                                                                                                                                                                                                                             Mus musculus (Mouse).
Eukaryota; Metazoa; Chordata;
Mammalia; Eutheria; Rodentia;
                                                                                                                                                                                                                                                                                                                                                                                                                                                     21-JUL-1986 (Rel. 01, Created)
21-JUL-1986 (Rel. 01, Last sequence update)
15-DEC-1998 (Rel. 37, Last annotation update)
SPERM PROTAMINE P1 (CYSTEINE-RICH PROTAMINE).
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Fungicide; Antibiotic.
SEQUENCE 33 AA; 4131 MW;
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"Purification and characterization of a novel antimicrobial peptide from maize (Zea mays L.) kernels.";
J. Biol. Chem. 267:18814-18820(1992).
-!- FUNCTION: INHIBITOR OF BOTH BACTERIAL AND FUNGAL GROWTH IN VITRO-!- TISSUE SPECIFICITY: PREDOMINANTLY IN THE EMBRYO PORTION OF THE
            This SWISS-PROT entry
                                                                                                                            STRAIN-C129;
                                                                                                                                                                                       SEQUENCE FROM N.A. MEDLINE=88181903;
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                               -!- SUBCELLULAR LOCATION: NUCLEAR.
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                                                                                                                                                                                                                                                                                                                                                  MEDLINE-85199803; PubMed=2986684; Kleene K.C., Distel R.J., Hecht N.B.; "Nucleotide sequence of a cDNA clone Biochemistry 24:719-722(1985).
                                                                                                                                                                      "Gene
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                                                                                                                                                                      expression
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Sci. 513:90-101(1987).
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EMBL; X14003; CAA32169.1; -.
EMBL; M27500; AAA39985.1; -.
EMBL; Z47352; CAA87410.1; -.
EMBL; Z47352; CAA87410.1; -.
PIR; A02660; HSMSS1.
PIR; S03820; S03820.
PIR; A28331; A28331.
MGD; MGI:97765; PRM1.
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P10118;
01-MAR-1989
                   Biol.
                                                                                                                                                            "Nucleotide sequence of a cDNA encoding rat protamine expression of the gene during rat spermatogenesis."; Biol. Chem. Hoppe-Seyler 370:293-301(1989).
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SPERM PROTAMINE P1 (CYSTEINE-RICH
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entities
                                                                                                    MEDLINE=96341725; PubMed=8720108;
Schlueter G., Cellk A., Obata R., Sc
Schlung A., Adham I.M., Engel W.;
"Sequence analysis of the conserved
                                                                                                                                                                                                                                            Rattus norvegicus (Rat).
Eukaryota; Metazoa; Chordata;
Mammalia; Eutheria; Rodentia;
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PROSITE; PS00048; PROTAMINE_P1;
Chromosomal protein; Nucleosome
SEQUENCE OF
                            "Rat sperm
                                      MEDLINE=89207111; PubMed=3072011; Ammer H., Henschen A.;
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or send an email to license@isb-sib.ch).
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Dev. 43:1-6(1996).
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30-MAY-2000 (Rel. 39, Last annotation update)
CAMP-DEPENDENT PROTEIN KINASE CATALYTIC SUBUNIT
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-!- FUNCTION: PROTAMINES SUBSTITUTES FOR HISTONES IN THE CHROMATIN (
-!- FUNCTION: PROTAMINES SUBSTITUTES FOR HISTONES IN THE CHROMATIN (
-!- SUBUNIT: CROSS-LINKED BY INTERCHAIN DISULFIDE BONDS AROUND THE
         of Dictyostel
Biochemistry
                                                                                                                                                                                   Dictyostelium discoideum (Slime mold)
Eukaryota; Dictyosteliida; Dictyostel
                                                                                              during Dictyostelium discoideum Gene 102:57-65(1991).
                                                                                                                                               SEQUENCE FROM N.A. MEDLINE=91323730; PubMed=1864510;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  MEDLINE=76184789; PubMed=1268226; Kistler W.S., Keim P.S., Heinriks
                                              Anjard C.,
                                                        MEDLINE=93385090; PubMed=8373760;
                                                                       CHARACTERIZATION
                                                                                                                      Buerki E., Anjard C., Scholder J.-C., Reymond C.D. "Isolation of two genes encoding putative protein
                                                                                                                                                                                                                                                                                     KAPC_DICDI
                                                                                                                                                                                                                                                                                                                                                                                                                                                              SEQUENCE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Chromosoma l
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        PFAM; PF00260; protamine_P1; 1.
PROSITE; PS00048; PROTAMINE_P1; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                INTERPRO;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              spermatozoa."
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        "Partial structural analysis
                                                                                                                                                                                                                                                                                                                                                 11
                    n unusual catalytic subunit for Dictyostelium discoideum.";
                                                                                                                                                                                                                                                                                                                                                                        σ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           TISSUE SPECIFICITY: TESTIS.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          SUBCELLULAR LOCATION: NUCLEAR.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            ; Z46939; CAA87061.1;
A27128; A27128.
S03997; S03997.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    DNA-HELIX (BY SIMILARITY)
                                                                                                                                                                                                            OR PK2 OR PK3.
                                                                                                                                                                                                                                                                                                                                                                       QTECQQCQRRCRQQESGPRQQQYCQRRCKEICEEEEEY 43
                                                                                                                                                                                                                                                                                                                                                RSRCRRRRRCRR-----RRRRCCRRRRRCCRRRRSY 43
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  DNA
                                                                                                                                                                                                                                                                                                                                                                                                Similarity 28.1
11; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 IPR000221;
                                              Etchebehere L.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                condensation;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             protein;
          32:9532-9538(1993)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                           36
37
                                                                                                                                                                                                                                                                                                                                                                                                                                                              AΑ;
                                                                                                                                                                                                                                                                                     STANDARD;
                                                                                                                                                                                                                                                                                                                                                                                                                                                              6889
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14
21
47
                                                                                                                                                                                                                                                                                                                                                                                                          25.6%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Nucleosome core; Spermatogenesis;
                                                                                                                                                                                                                                                                                                                                                                                                                                                            ₩.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Heinrikson
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Nuclear protein
                                                                                                                                                                                     Dictyostelium
                                                                                                                                                                                                                                                                                                                                                                                              score 63.5; 1; Pred. No. 0.8; 11; Mismatches
                                              Pinaud
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         of
                                                                                                                                                                                                                                                                                                                                                                                                                                                           INTERCHAIN (WITH CYS-5)
INTERCHAIN (WITH CYS-36
BY SIMILARITY.
B60B9F3D1BB6D978 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            INTERCHAIN (WITH BY SIMILARITY.
                                                                                                                                                                                                                                                                                     PRT;
                                                                                                          development.";
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         the
                                 S.,
the
                                                                                                                                                                                                                                                                                                                                                                                                         No. 0.
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basic chromosomal
                                                                                                                                                                                                                                                                                   648
                                              Veron M.,
                                 cAMP-dependent
                                                                                                                                                                                                                                                                                   ΑA
                                                                                                                                                                                                                                                                                                                                                                                                           . 88;
                                                                                                                                                                                                                                                                                                                                                                                                                        DB
                                                                                                                                                                                                                                                                                                                                                                                                                      1;
                                                                                                                                                                                                                                                                                                                                                                                                 11;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  CYS-36)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        CYS-21)
                                              Reymond C.D.;
                                                                                                                                                                                                                          (EC
                                                                                                                                                                                                                                                                                                                                                                                                                       Length 50
                                                                                                                      kinases regulated
                                                                                                                                                                                                                                                                                                                                                                                                 Indels
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                                 protein kinase
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        (BY SIMILARITY)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             DNA-binding;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                SIMILARITY)
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Best Local
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                                                                         ANDR_CANFA
Q9TT90;
30-MAY-2000
30-MAY-2000
30-MAY-2000
Mammalia; [1]
                                                                                                                                                                                                                                                                                                                ACT_SITE
MOD_RES
SEQUENCE
                                   ANDROGEN RECEPTOR (DIH
AR OR NR3C4.
Canis familiaris (Dog)
                                                                                                                                                                                                                                                                                                                                                      NP_BIND
BINDING
                                                                                                                                                                                                                                                                                                                                                                                          DOMAIN
DOMAIN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    EMBL;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               "DdPK3, which plays essential roles during Dictyostelium encodes the catalytic subunit of cAMP-dependent protein Proc. Natl. Acad. Sci. U.S.A. 89:10701-10705(1992).
                                                                                                                                             CANFA
                                                                                                                                                                                                                                                                                                                                                                                                                    Phosphorylation.
DOMAIN 58
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        DICTYDB; DD02030; PKAC.
INTERPRO; IPR000719; -.
INTERPRO; IPR000961; -.
INTERPRO; IPR002290; -.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               This SWISS-PROT entry is copyright. It is produced through a between the Swiss Institute of Bioinformatics and the EMBI the European Bioinformatics Institute. There are no restrict
                         Eukaryota; Metazoa;
                                                                                                                                                                                                                                                                                                                                                                                                                                                          PROSITE; PS00108; PROTEIN_KINASE_ST; 1 PROSITE; PS50011; PROTEIN_KINASE_DOM;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               PFAM; PF00069; pkinase; 1. PFAM; PF00433; pkinase_C;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          modified and this statement is not removed. entities requires a license agreement (See
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              STRAIN-AX3
                                                                                                                                                                                                                                                                                                                                                                               DOMAIN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  PROSITE; PS00107; PROTEIN_KINASE_ATP;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             HSSP;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              or send an email to license@isb-sib.ch).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Mann S.K.O.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              CHARACTERIZATION
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    MEDLINE=93066311; PubMed=1332055;
                                                                                                                                                                                               Local
                                                                                                                                                                                                                       2 QEDPQTECQQCQRRCRQQESGPRQQQYCQRRCKEICEEEEE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      FUNCTION: ESSENTIAL FOR DIFFERENTIATION AND FRUIT MORPHOGENESIS.
CATALYTIC ACTIVITY: ATP + A PROTEIN = ADP + A PHOSPHOPROTEIN.
SUBUNIT: IN DICTYCOSTELLUM THE HOLDENZYME IS A DIMER COMPOSED OF
A REGULATORY (R) AND A CATALYTIC (C) SUBUNIT: IN THE PRESENCE OF
CAMP IT DISSOCIATES INTO THE ACTIVE C SUBUNIT AND AN R MONOMER.
DEVELOPMENTAL STRAGE: CAPK ACTIVITY IS LOW IN VECETATIVELY GROWIN.
BANGEBAE, INCREASES DUBLING DEVELOPMENT OF AGGREGATION AND REACHES
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    CAMP SUBFAMILY
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               SIMILARITY: BELONGS TO THE SER/THR FAMILY OF PROTEIN KINASES
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        JQ
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            7Q1150; JQ1150.
P05132; 2CPK.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    M38703; -; NOT_ANNOTATED_CDS
                                                                                                                                                                                                                                                               Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    non-profit
          Eutheria;
                                                                                                                                                                                                                                                                                                                  648
                                                                            (Rel.
(Rel.
(Rel.
                                                                                                                                                                                                                                                  Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                            Serine/threonine-protein kinase; ATP-binding; cAMP;
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                                                                                                                                                                                                                                                                                                                  AA;
                                                                                                                                                                                                                                                                                                         64
223
250
590
350
365
459
459
479
                                                                                                                               STANDARD;
                                                             39, Created)
39, Last sequence update)
39, Last annotation update)
(DIHYDROTESTOSTERONE RECEPTOR).
            Carnivora;
          Chordata; Craniata; Vertebrata; Euteleostomi; Carnivora; Fissipedia; Canidae; Canis.
                                                                                                                                                                                                                                                               25.0%;
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                                                                                                                                                                                                                                                                                                                 MW,
                                                                                                                                                                                                                                                  15;
                                                                                                                                                                                                                                                 Score 62; DB
Pred. No. 9.6;
l5; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Taylor S.S.,
                                                                                                                                                                                                                                                                                                                                                                                          ASN-RICH.
GLN-RICH.
THR-RICH.
                                                                                                                                                                                                                                                                                                                          PROTEIN KINASE.
ATP (BY SIMILARITY).
ATP (BY SIMILARITY).
BY SIMILARITY.
PHOSPHORYLATION (BY SIMILARITY).
                                                                                                                               PRT;
                                                                                                                                                                                                                                                                                                                  D0F9B3A48C58D084 CRC64;
                                                                                                                               907
                                                                                                                                                                                                                                                                          DB 1; Length 648
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      as its content
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            http://www.isb-sib.ch/announce/
                                                                                                                                                                                                                                                  14;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Usage
                                                                                                                                                                                                                         42
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                                                                                                                                                                                                                                                  Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Ьy
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                restrictions
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L outstation -
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Best Local S
Matches 13
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           androgen receptor.";
Submitted (OCT-1999) to the EMBL/GenBank/DDBJ databases.
-i- FUNCTION: THE STEROID HORMONES AND THEIR RECEPTORS ARE I
THE REGULATION OF EUKARYOTIC GENE EXPRESSION AND AFFECT
PROLIFERATION AND DIFFER
                                                                        "Complete sequence of ovine alpha s2-casein messenger RNA.", Biochimie 67:1043-1051(1985).
                                                                                                                                                                                                          Ovis aries (Sheep).
Eukaryota; Metazoa; Chordata; Crania
Mammalia; Eutheria; Cetartiodactyla;
                                                                                                                                                                                                                                                                                         13-AUG-1987 (Rel. 05, Crea
13-AUG-1987 (Rel. 05, Last
01-NOV-1997 (Rel. 35, Last
ALPHA-S2 CASEIN PRECURSOR.
                                                                                                                                                                                                                                                                                                                                                                                                              SHEEP
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           DOMAIN
DOMAIN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          DNA_BIND
                                                          -
                                                                                                                         SEQUENCE FROM N.A.
MEDLINE=86104467; PubMed=3002499;
                                                                                                                                                                                                                                                                          CSN1S2
                                                                                                                                                                                                                                                                                                                                                                                        CAS2_SHEEP
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   This
                                                                                                               Boisnard M., Petrissant G.;
                                                                                                                                                                                                                                                                                                                                                                       P04654;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Zinc-finger;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Receptor; Transcription regulation;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      entities
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                SEQUENCE
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             s
CALCIUM PHOSPHATE.
SUBCELLULAR LOCATION:
TISSUE SPECIFICITY: M/
                                                      FUNCTION: IMPORTANT ROLE IN THE CAPACITY
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    SUBCELLULAR LOCATION: NUCLEAR,
DOMAIN: COMPOSED OF THREE DOMAINS: A MODULATING N-TERMINAL D
A DNA-BINDING DOMAIN AND A C-TERMINAL STEROID-BINDING DOMAIN
SIMILARITY: BELONGS TO THE NUCLEAR HORMONE RECEPTORS FAMILY.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             European
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            NR3 SUBFAMILY.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   SWISS-PROT entry is copyright. It is produced through sen the Swiss Institute of Bioinformatics and the Emburopean Bioinformatics Institute. There are no restr by non-profit institutions as long as its content
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   l Similarity
13; Conserv
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  an email to license@isb-sib.ch)
                                                                                                                                                                                            Caprinae;
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547
583
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131
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329
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                                                                                                                                                                                                                                                                                                                                                                                          STANDARD;
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                                                                                                                                                                                            Ovis.
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567
607
907
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76
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332
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  98726 MW;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      license
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      24
48
                                                                                                                                                                                                                                                                                                         Last sequence up
                                                                                                                                                                                                                                                                                                                                                 Created)
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  MAMMARY
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                                                                                                                                                                                                                                                                                                                                                                              SEQUENCE FROM N.A. MEDLINE=90348475; PubMed=2385171;
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Eukaryota; Metazoa; Cho
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     or send an email to license@isb-sib.ch).
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Biol. Evol. 7:293-302(1990).

FUNCTION: INVOLUCRIN IS A KERATINOCYTE PROTEIN THAT FIRST APPEA IN THE CELL CYTOSOL, BUT ULTIMATELY BECOMES CROSS-LINKED TO MEMBRANE PROTEINS BY TRANSGLUTAMINASE. ALL THAT RESULTS IN THE FORMATION OF AN INSOLUBLE ENVELOPE BENEATH THE PLASMA MEMBRANE. TISSUE SPECIFICITY: PRESENT IN KERATINOCYTES OF EPIDERMIS AND OTHER STRATIFIED SQUAMOUS EPITHELIA.
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Submitted (AUG-1998) to the EMBL/GenBank/DDBJ databases.

Submitted (AUG-1998) to the EMBL/GenBank/DDBJ databases.

THETION: ORPHAN RECEPTOR. INTERACTION OF LXR ALPHA WITH RXR SHIFTS RXR FROM ITS ROLE AS A SILENT DNA-BINDING PARTNER TO ACTIVE LIGAND-BLNDING SUBUNIT IN MEDIATING RETINOID RESPONSE THROUGH TARGET GENES DEFINED BY LXRES (BY SIMILARITY).

THROUGH TARGET GENES DEFINED BY LXRES (BY SIMILARITY).

THROUGH TARGET GENES DEFINED BY LXRES (BY SIMILARITY).
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ZN_FING
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INTERPRO; IPR000536; -.
INTERPRO; IPR001628; -.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entitles requires a license agreement (See http://www.isb-sib.ch/announce/or send an email to license@isb-sib.ch).
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Mus musculus (Mouse).
Eukaryota; Metazoa; (
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            OXYSTEROLS RECEPTOR LXR-ALPHA (LIVER
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                30-MAY-2000 (Rel.
30-MAY-2000 (Rel.
30-MAY-2000 (Rel.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Q9Z0Y9;
30-MAY-2000
                                                                                                                                                                                                                                                                                                                                             Receptor; Transcription regulation;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             NR1H3 OR LXRA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  RECEPTOR LXR-ALPHA).
                                                                                                                                                                                                                                                                                                                         Zinc-finger.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    NRH3_MOUSE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           142 QQQEQQESQEKELHLEQEQQKEELQQQEQQQGKEQCEKHQE 182
147
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    2 QEDPQTECQQCQRRCRQQESGPRQQQYCQRRCKEICEEEEE 42 | : | | | | : : | | | | | : : |
                                              8 ECQQCQ-RRCRQQESGPRQQQYC----QRRCKEICEEEEE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  NR1 SUBFAMILY.
KCQECRLRKCRQ--AGMREE--CVLSEEQIRLKKLKRQEEE
                                                                                                                                                                                                                                                                                                                                                                                                                     PF00104; hormone_rec; PF00105; zf-C4; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          AF085745; AAD16050.1; P20393; 1A6Y.
                                                                                               16; Conser
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Similarity
13; Conser
                                                                                                                                                                                                                       445
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                                                                                                 Conservative
                                                                                                                                                                                                                                                                        96
96
                                                                                                                                                                                                                       ΑĄ;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    STANDARD;
                                                                                                                                                                                                161
116
156
50417,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           39, Created)39, Last sequence update)39, Last annotation update
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Chordata;
Rodentia;
                                                                                                                 23.8%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 23.8%;
                                                                                                                                                                                                                       WW.
                                                                                               10;
                                                                                                                                                                                                                                            C4-TYPE ZINC C4-TYPE. C4-TYPE.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            9;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Score 59;
Pred. No.
                                                                                                                   Score 59; DB
Pred. No. 14;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Pred. No. 10;
); Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Craniata; Vertebrata; Euteleostomi; Sciurognathi; Muridae; Murinae; Mus.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       PRT;
                                                                                                                                                                                                                       1A426DF38D935731 CRC64
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     DCE1BD88B9248BEA CRC64;
                                                                                                 Mismatches
                                                                                                                                                                                                                                                                                                                                             DNA-binding; Nuclear protein;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              ×
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x receptor alpha) (NUCLEAR ORPHAN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            DB
10;
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                                                                                                                                             1;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            19;
                                                                                               5.
                                              42
                                                                                                                                               Length 445;
183
                                                                                                 Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               RESPONSES
                                                                                               10;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            0
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RESULT IN RESULT
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Q1313;
30-MAY-2000 (Rel. 39, Created)
30-MAY-2000 (Rel. 39, Last sequence up
30-MAY-2000 (Rel. 39, Last annotation
                                                                                                                                                                                                                                                                        DNA_BIND
ZN_FING
ZN_FING
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation the European Bioinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Genes Dev. 9:1033-1045(1995).

-i- FUNCTION: ORPHAN RECEPTOR. INTERACTION OF LXR ALPHA WITH RXR SHIFTS RXR FROM ITS ROLE AS A SILENT DNA-BINDING PARTNER TO A ACTIVE LIGAND-BINDING SUBUNIT IN MEDIATING RETINOID RESPONSES
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     EMBL; U22662; AAA85856.1; HSSP; P20393; 1A6Y. MIM; 602423; -.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    RECEPTOR LXR-ALPHA). NR1H3 OR LXRA.
                                                                                                                                                                                                                                                  SEQUENCE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           entities requires a license agreement (See http://www.isb-sib.ch/announce/or send an email to license@isb-sib.ch).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Willy P.J., Umeso Mangelsdorf D.J.;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               MEDLINE=95262897; PubMed=7744246; Willy P.J., Umesono K., Ong E.S.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Eukaryota; Metazoa;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Homo sapiens (Human).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        OXYSTEROLS RECEPTOR LXR-ALPHA (LIVER X RECEPTOR ALPHA) (NUCLEAR ORPHAN
                                                                                                                                                                                                                                                                                                                                                           Zinc-finger.
                                                                                                                                                                                                                                                                                                                                                                                                       PRINTS; PRO0047; STROIDFINGER. PROSITE; PS00031; NUCLEAR_RECEPTOR;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                 PFAM; PF00104; hormone_rec; PFAM; PF00105; zf-C4; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             pathway
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            TISSUE=LIVER
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Mammalia; Eutheria;
           149
                                                                                                                                                                                                                                                                                                                                                                                    Receptor;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   INTERPRO; IPR000536; INTERPRO; IPR001628;
                                                         8 ECQQCQ-RRCRQQESGPRQQQYC----QRRCKEICEEEEE 42
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                SUBCELLULAR LOCATION: NUCLEAR (POTENTIAL).
INDUCTION: BY 9-CIS RETINOIC ACID (9CRA).
SIMILARITY: BELONGS TO THE NUCLEAR HORMONE RECEPTORS FAMILY
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             THROUGH TARGET GENES DEFINED BY LXRES SUBUNIT: INTERACTS WITH RXR.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          NR1 SUBFAMILY.
KCQECRLRKCRQ--AGMREE--CVLSEEQIRLKKLKRQEEE 185
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                a nuclear receptor that defines a distinct retinoid
                                                                                                              l Similarity
16; Conserv
                                                                                                                                                                                                                                                                                                                                                                                       Transcription
                                                                                                                                                                                                                                             98
98
134
447
                                                                                                                 Conservative
                                                                                                                                                                                                                                                     AA;
                                                                                                                                                                                                                                                                        163
118
158
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Chordata;
Primates;
                                                                                                                                            23.8%;
                                                                                                                                                                                                                                                     50480 MW;
                                                                                                                                                                                                                                                                                                                                                                                    regulation;
                                                                                                                 10;
                                                                                                                                                                                                                                                                           C4-TYPE ZINC
C4-TYPE.
C4-TYPE.
                                                                                                                                                                  Score 59;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Craniata; Vertebrata; Euteleostomi; Catarrhini; Hominidae; Homo.
                                                                                                                                                                                                                                                     A227B233DB0F8C96 CRC64;
                                                                                                                 Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Evans R.M., Heyman R.A.
                                                                                                                                            No.

    DNA-binding; Nuclear protein;

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                                                                                                                                                                                                                                                                                                                                  FINGERS
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                                                                                                                                                                     Length 447;
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                                                                                                                 Indels
                                                                                                                                                                                                                                                                                                                                  (TWO)
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                                                                                                                 10;
                                                                                                                 Gaps
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